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TECH CENTER 1800/2900 TRANSMITTAL FORM (for all correspondence after initial filing)	Attorney Docket No. MBA-101	Total Pages
	Application Number 09/847,513	
	Filing Date 5/1/2001	
	First Named Inventor EDWARD F. DELONG	
	Group Art Unit 1645	
	Examiner NOT ASSIGNED	

ENCLOSURES (check all that apply)	
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<input checked="" type="checkbox"/> Response/Amendment	<input type="checkbox"/> Assignment papers
<input checked="" type="checkbox"/> Reply under 37 CFR 1.111 with mark up version and clean version	<input type="checkbox"/> Power of Attorney by Assignee
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<input checked="" type="checkbox"/> Corrected sequence listing Total Sheets: [235]	<input type="checkbox"/> with copies of cited references
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SIGNATURE OF AGENT	
NAME	MAREK ALBOSZTA, REG. NO. 39,894
Signature	
Date	6 Aug. 2001

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I hereby certify that this correspondence is being deposited on the date indicated below as first class mail with the U.S. Postal Service addressed to the ASSISTANT COMMISSIONER FOR PATENTS, WASHINGTON, DC 20231.	
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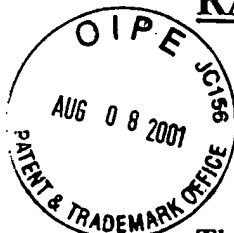
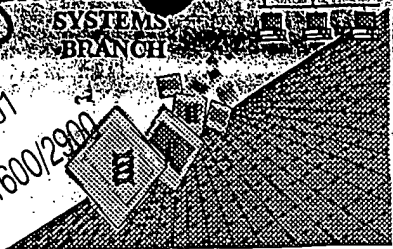
Received
June 11, 2001

BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING ERROR REPORT

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TECH CENTER 1600/2900



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/847,513
Source: OIPE
Date Processed by STIC: 5/16/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

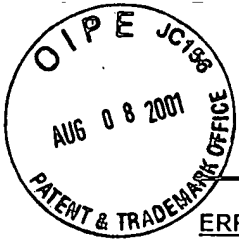
The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>



09847513 .080801

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTIONSERIAL NUMBER: 09/847,573

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped
- Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/847,513

DATE: 05/16/2001
TIME: 13:37:02

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Output Set: N:\CRF3\05162001\I847513.raw

Does Not Comply
Corrected Diskette Needed

pp. 21⁶

3 <110> APPLICANT: MBARI
4 DeLong, Edward
5 Beja, Oded
7 <120> TITLE OF INVENTION: Light-driven energy generation using proteorhodopsin
9 <130> FILE REFERENCE: MBA-101
--> 11 <140> CURRENT APPLICATION NUMBER: US/09/847,513
--> 11 <141> CURRENT FILING DATE: 2001-05-01
11 <150> PRIOR APPLICATION NUMBER: 60/201,602
12 <151> PRIOR FILING DATE: 2000-05-03
14 <160> NUMBER OF SEQ ID NOS: 65
16 <170> SOFTWARE: PatentIn version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 105184
20 <212> TYPE: DNA
21 <213> ORGANISM: Naturally occurring gamma proteobacterium
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--> 24 <221> NAME/KEY: CDS(complement)
25 <222> LOCATION: (50866)..(51615)
26 <223> OTHER INFORMATION: light-driven proton pump; has the properties of a light-driven pr
27 oton pump when expressed with retinal in Escherichia col
30 <300> PUBLICATION INFORMATION:
31 <301> AUTHORS: Beja, O., Aravind, L., Koonin, E.V., Suzuki, M.T., Hadd, A., Nguyen, L.P.,
32 Jovanovich, S.B., Gates, C.M., Feldman, R.A., DeLong, E.F
33 <302> TITLE: Bacterial rhodopsin: evidence for a new type of phototrophy in the sea
34 <303> JOURNAL: Science
35 <304> VOLUME: 289
36 <305> ISSUE: 5486
37 <306> PAGES: 1902-1906
38 <307> DATE: 2000-09-15
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40 <309> DATABASE ENTRY DATE: 2000-06-15
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PATENT APPLICATION: US/09/847,513

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see

Jim 10 on

Eva summary
sheet

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RAW SEQUENCE LISTING

DATE: 05/16/2001

PATENT APPLICATION: US/09/847,513

TIME: 13:37:02

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286	ttttcagatg	aacagctaca	aattttataat	attgtccaca	aagccaatct	tgctgcaatc	7320
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292	ggtgcattca	aggactttta	tatgcataag	gtgggacatt	ggcttggaat	tgatgttcat	7500
294	gatgttggtg	actacatgga	gggagatgag	tttatgaagt	ttaagccagg	gatgataacc	7560
296	acaatcgagc	caggcaatga	tatcagtagc	gcaatggatg	tagatgacaa	atggaaaggc	7620
298	atcggcataa	gaatagagga	cgacatcctt	gtaacagatt	caggcaatat	taatctaaca	7680
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302	ccaattgtta	tttctggcgg	agggataata	ggtaattaca	tttctcttag	gcttgaaaaa	7800
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306	ataagaacag	tcactctcaa	tgagcattct	atgcacatgc	taaaaaatat	tggtatttgc	7920
308	coatcaattg	ctcaaatcaa	cagcatcgac	gtattagatg	gtgagggtac	aggcaaaatt	7980
310	caatttctag	caaaggacgt	aggcagcgaa	aacctttcat	atgtaacctt	tttcaatgaa	8040
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314	tcagttcaga	atcttaatac	agaatctgat	ccagagatca	tgcttaaaga	tggtatgacc	8160
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318	tcacttacaa	gcagcttcga	tgactactta	caaacagctt	taacttttgt	cgttgatatt	8280
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326	gaatcaaaag	ttaatgttag	tctcagggtt	aagtcagaaa	ttttaagttt	taaattatcg	8520
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340	aataagtttt	aaatttgtat	taaacttttt	gaccttttag	tctaagttct	ttaagaactt	8940
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344	acctgttctc	agattcaacc	caaaatttgt	gtgtgtgaag	attaggaaaa	aactttcttt	9060
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RAW SEQUENCE LISTING

DATE: 05/16/2001

PATENT APPLICATION: US/09/847,513

TIME: 13:37:02

Input Set : A:\MBA10101.txt

Output Set: N:\CRF3\05162001\I847513.raw

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372 gtacttagaa gatcccggtc ttgcagcaat ggttatacct agatcagggt taggttctaa 9900
374 gcatggaatc gttcttggtg atctggttgg gttgattgat tcagactatc aaggagagct 9960
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```


09/847,513_6

<210> 4
<211> 750
<212> DNA
<213> Naturally occurring gamma proteobacterium

<220>
<221> CDS
<222> (1)..(750)
<223> light-driven proton pump; has the properties of a light-driven proton pump when expressed with retinal in Escherichia coli. Note that additional three nucleotide residues incorporated by pcr priming with reference to the original 31A08 DNA sequence (DNA residues 4-6, ggt), adding a new restriction site for cloning

→
FYI: Per 1.823 of Sequence Rules, the <223> response has a MAXIMUM of 4 lines.

VERIFICATION SUMMARY

DATE: 05/16/2001

PATENT APPLICATION: US/09/847,513

TIME: 13:37:03

Input Set : A:\MBA10101.txt

Output Set: N:\CRF3\05162001\I847513.raw

:11 M:270 C: Current Application Number differs, Replaced Current Application No
:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
:24 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
:3559 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
:3572 M:286 W: Invalid Database Entry: Valid Formats YYYY-MM-DD or Mon-YYYY, SEQ ID:2
:3584 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
:3597 M:286 W: Invalid Database Entry: Valid Formats YYYY-MM-DD or Mon-YYYY, SEQ ID:3
:3615 M:259 W: Allowed number of lines exceeded, <223> Other Information:
:3790 M:286 W: Invalid Database Entry: Valid Formats YYYY-MM-DD or Mon-YYYY, SEQ ID:6